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Listing first 45 summaries
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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264 SFAERFSKMATKTLLVTVSDYVHLPAYKRWYRKFKEFIVN-FFTDPAKLIMKHVSQPVKT 322 KFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLKNFMVNRVFIPTKKFFNKEIREPSK- 302

Qy 64 Db 93 Qy 124 Db 147 Qy 184 Db 205	Keywor Query Query Best I Matche	A; Cross-refe A; Experiment A; Note: sequ R; Mishra, V. Mol. Biochem A; Title: Isc A; Reference A; Accession: A; Molecule t A; Molecule t A; Residues: A; Note: sequ C; Genetics: A; Gene: p58	RESULT 1 A45614 merozoite C:Species: C:Date: 22 C:Accessio R:Mishra, Mol. Bioch A:Title: I A:Referenc A:Recessio A:Molecule A:Residues	30 32 32 33 33 33 33 33 33 34 40 40 40 11
SAYMSRCAKODCLTLQSLK :: : : : : : : : : : : :	ords: surface antige ords: surface antige y Match Local Similarity hes 181; Conservat 4 SDSVGDVTKTLLAASE :: :	Cross references: EMBL:M6087 Experimental source: merozoil Note: sequence extracted fro Mishra, V.S.; McElwain, T.F.)1. Biochem. Parasitol. 53, 1 Title: Isolation, sequence a Reference number: A45561; MU Accession: A45561 Molecule type: DNA Molecule type: DNA Residues: 1-281,'G', 283-480 Note: sequence extracted fro Gene: p58	RESULT 1 A45614 A45614 C;Species: Babesia bigem C;Date: 22-Apr-1993 #seg C;Accession: A45614; A45 R;Mishra, V.S.; Stephens Mol. Biochem. Parasitol. A;Title: Immunogenicity A;Reference number: A456 A;Accession: A45614	113.5 4.112.5 4.111.5
DCLTLQSLKYP CLTLDSM PYFHDLVFNLLE CTHEVESLLE CTHEVESLE CTHEVESLE	antigen 35.1% 11.8% ity 41.8% servative LLAASESVDSA : :	ss: EMBL:M60878 wrrce: merozoit extracted from foElwain, T.F.; foElwain, T.F.; asitol. 53, 14 asitol. 53, 14 asitol. 54, 14 asitol. 57, 14 a	tigen p58 - igemina #sequence_r #sequence_r A45561; S2 hens, E.B.; tol. 47, 20 ity and seq a45614; MUI	8 252 2 8 2364 2 8 1314 2 7 1957 2 7 1957 2 7 1812 2 7 1812 2 7 6359 2 7 6359 2 7 1271 2 1076 2 6 1939 2 6 1939 2
LEAKYQPLTLPDDYQLEAAFILFKE : : : : : : : : : : : : :	Surface antigen Surface antigen 35.1%; Score 827.5; DB 1; Length 480; ch 1 Similarity 41.8%; Pred. No. 1.6e-46; 181; Conservative 75; Mismatches 140; Indels 37; 181; Conservative 75; Mismatches 140; Indels 37; 181; Conservative 15; High 15; Hig	; NID:g155860; PIDN:AAA6558 e NCBI backbone (NCBIN:65037 Dame, J.B.; Stephens, E.B. g-158, 1992 d differential expression o D:92365724 MIS2> NCBI backbone (NCBIN:11116	RESULT 1 A45614 Merozoite surface antigen p58 - Babesia bigemina C;Species: Babesia bigemina C;Cacession: A45614; A45561; S27775 R;Mishra, V.S.; Stephens, E.B.; Dame, J.B.; Perryman, L.E.; Mol. Biochem. Parasitol. 47, 207-212, 1991 A;Title: Immunogenicity and sequence analysis of recombinant A;Reference number: A45614; MUID:92049553 A;Residues: 1-480 <misi></misi>	F90561 A26655 A366577 A856577 A856577 T50382 T50382 G90576 A46417 T20333 T20333 T20333 T3679 HMIV T43207 D64237 D64237 D84687 T18372 B718372 ALIGNMENTS
	gth 480; els 37; Gaps 12; QVPKGSNCSASV 63 : KVAGNSTCGESV 92	3.1; PID:g155861 , NCBIP:65038) f the p58 gene family of Ba	hange 16-Jul-1999 ; McGuire, T.C.; McElwain, nt p58: a neutralization-se	hypothetical prote myosin heavy chain microtubule-associ hypothetical prote hypothetical coile probable spindle p heat shock atp-dep NIP1 protein - yea hypothetical prote bacitracin synthet hemagglutinin prec nuclear fusion prote hypothetical prote probable kinesin-l repeat organellar hypothetical prote

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merozoite surface antigen, 6
C;Species: Babesia bovis
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C;Accession: S27778
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A;Description: Characterization of the gene encoding a 60 kilodalton Babesia bovis
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;Superfamily: merozoite surface antigen p58
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Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 17-Nov-2000
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   SDSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCSASV
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R;Mishra, V.S.; McElwain, T.F.; Dame, J.B.; St Mol. Blochem. Parasitol. 53, 149-158, 1992 A;Title: Isolation, sequence and differential A;Reference number: A45561; MUID:92365724 A;Accession: D45561
                                                                                                         A;Cross-references: GB:M85187
C;Superfamily: merozoite surf
                                                                                                                                                                                                                                                                                                                                            merozoite surface antigen (clone 14) - Babesia C;Species: Babesia bigemina C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1
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A;Accession: B45561
A;Status: preliminary
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C;Date: 09-Sep-1994 #sequence_revision
C;Accession: B45561
                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-480 <MIS>
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A; Residues: 1-442 <MIS>
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                                                                                    surface antigen
                      Similarity
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Score 813.5; DB 2
Pred. No. 1.3e-45;
4; Mismatches 142
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Pred. No. 2.9e-46;
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1992
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merozoite surface antigen (clone 9) - Babesia bigemina C;Species: Babesia bigemina C;Species: Babesia bigemina C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_C;Caccession: C45561
R;Mishra, V.S.; McElwain, T.F.; Dame, J.B.; Stephens, E.B. Mol. Biochem. Parasitol. 53, 149-158, 1992
A;Title: Isolation, sequence and differential expression A;Reference number: A45561; MUID:92365724
A;Accession: C45561
A;Status: preliminary
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C45561
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C;Keywords: surface antigen
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C;Superfamily: merozoite surface antigen
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A; Residues: 1-442 <MIS>
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Matches 170
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SFAEAFSKMATKTLLVTVSDYVHLPAYKRWYRKFKEFIVN-FFTDPAKLIMKHVSQPVKT
                        KFAKRESLMVVQRLLATVAGYVDTPWYKKWYMKLKNFMVNRVFIPTKKFFNKEIREPSK-
                                                                   FFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIPALP
                                                                                                                       MRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLYYKTYTNVDEFGAS
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                                                                                                          MRSR--SSHGDYHHFVVSLLKKNVVRDPESNDVENFASQYFYMTTLYYKTYLTVDFTAAK
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                                                                                                                                                                                                                                                                                      Score 790;
Pred. No.
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rhoptry protein homolog Bc60.2 - Babesia canis
C;Species: Babesia canis
C;Species: Babesia canis
C;Bate: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: C48572
R;Dalrymple, B.P.; Casu, R.E.; Peters, J.M.; Dimmock, C.M.; Gale, K.R.; Boes
Mol. Biochem. Parasitol. 57, 181-192, 1993
A;Title: Characterisation of a family of multi-copy genes encoding rhoptry parasitol. 57, 181-192, 1993
A;Reference number: A48572; MUID:93165069
A;Accession: C48572
A;Status: preliminary
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A; Residues: 1-456 < DAL>
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LENEAVEDGQLTMGDVTDFEMATPTYEQGSQESLNEVGNE
                                    FENKI----GQGTV-DFINKEIRDP-----SKALIRKVSTE
                                                                         EFFVNKLHEPTKEFFSNMVPGAFQKISEKAGR--
                                                                                                          DFINNEIRDPSKALIRKVSTGAEDLFENKIGQGTVDFINNEIRDPSKALIRKVYTEADDL
                                                                                                                                                                   SKALKEKVSTDTKDLFENKIGQGTVDFFNKEIRDPSKALKEKVSNDAKDLFENKIGQGTV
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                                                                                                                                                                                                                                                                                                                                                                         AFWMRFRHGGRYGAYHNFLVNILYKNLSDSMVDDNLEGFVRKYAYMATMYYKTYTALDVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEK
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Pred. No. 7.8e-43;
5; Mismatches 161;
                                                                         ---HLRS-SKTVVPE--DEPSSS
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RESULT 7
A48572
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C;Species: Babesia ovis
C;Species: Babesia ovis
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A48572
R;Dalrymple, B.P.; Casu, R.E.; Peters, J.M.; Dimmock, C.M.; Gale, K.R.; Boes Mol. Biochem. Parasitol. 57, 181-192, 1993

Boese,

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RESULT 9
T28411
ORF MSV250
C; Species:
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A; Note:
C; Superf
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A; Residues: 1-321 <DAL>
A; Cross-references: GB:M91173
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A; Reference number:
A; Accession: A48572
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A; Residues: 1-192 <DAL>
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                                                                                                                                                                                                                                                                                                                                                      sequence inconsistent with the nucleotide translation sequence extracted from NCBI backbone (NCBIN:125078, | family: merozoite surface antigen p58
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                                                                                              GQWMRFRNGKKHGDYHRFLIGLLAKGVTRKDGATDLE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYMATTYYKTYLIVNNSDAKFFNRIAFATKIFGFGIKKALKDIVRSNVPEYMG-EHSIER 60
                                                                                                                                                                                                                         LAPAEVVGNVAATLSTADEIISSHDYDKELINDMRDQMREMGENFVDTVCTKAPEDSNCR 90
                                                                                                                                                                                                                                                       MAPSDSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPERTKDFFENKLPEHTKDFFENKLPEHTKDFFENKIGAPIK 269
                                                                                                                            RFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIE
                                                                                                                                                                            ASVSAYMSRCAKODCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEK 120
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                                                                                                                                                            QMVALYADRCEMYGCLQIDNVNYPVDEEYQPLSLPNPYQLDAAFTLFKNSASNPAKNGVK 150
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 Melanoplus
             hypothetical protein
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sanguinipes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Babesia ovis
                                                                                                                                                                                                                                                                                       Score 366; DB 2;
Pred. No. 5.7e-17;
0; Mismatches 59
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Pred. No. 4.9e-34;
Melanoplus sanguinipes entomopoxvirus
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                                                                                                                                                                                                                                                                                            59;
                                                                                                                                                                                                                                                                                                                     Length 192
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              entomopoxvirus
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C;Date: 21-Jan-2000 #sequence_revision 21-Jan-C;Accession: T28411
R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.;
J. Virol. 73, 533-552, 1999
A;Title: The genome of Melanoplus sanguinipes
A;Reference number: Z20484; MUID:99102612
A;A;Accession: T28411
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A; Residues: 1-441 < AFO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references:
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Best Local (
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NKNVNDFVNKNVND
                                                                                    SKALIRKVSTGAEDLFENKIGQGTVDFINNEIRDPSKALIRKVYTEADDLFENKIGQGTV 430
                                                                                                                                                                      DTKDLFENKIGOGTVDFFNKEIRDPSKALKEKVSNDAKDLFENKIGOGTVDFINNEIRDP
                                                                                                                                                                                                                                          LMVVQRLLATVAGYVDTPWYKKWYMKLKNFMVNRVFIPTKKFFNKEIREPSKALKEKVST 310
                                                                                                                                                                                                                                                                                                                                                                                                                  -----DFYFDDYAFCEEHKFCQNHMN-YENGIWK-----ENYEYCYNICNECEESKIFK 180
                                                                                                                                     NVDD-FVNKIDD---DFVNK--
                                                                                                                                                                                                          NKVVNK - - - NVDNVVD - - - - - - EVVNKNVDKV - - - VNEVVNKNV - - - DKVVDEVVNK
                                                                  ---VVNKI----DDEFVNK
                                                                                                                                                                                                                                                                                                         TTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIPALPKFAKRFS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                   QPLTLPDPYQLEAAFILFKESDANPANSTEKRFWMRFRRGKNHSYFHDLV------ 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INSDMSDYLSAVSDNFAERICSQVPKGSNCSASVSAYMSRCAKQDCLTLQSLKYPLEAKY 89
                                ----DFINKEIRD
                                                                                                                                                                                                                                                                                                                                               FENKLENYTLLSKLLSSEITTTETVEN-----ANTIILPTKTONIDDDSEYFYDREIY
                                                                                                                                                                                                                                                                                                                                                                                -----FNLLEKNVTRDADATD-IENFASRYLYMATLYYKTYT-NVDEFGASFFNKLSF 190
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410
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                                                                                                                                                                                                                                                                            ----TMHENKDYDFINKVVDDYVDNYV---NKFVDDFV
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                                                                    - NVDEVVNK IDDVLNKNVNEVVNKDVNDFVNK IDDEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 143.5; DE Pred. No. 0.051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from GB/EMBL/DDBJ
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                                                                    396
                                                                                                                                                                                                                                                                            269
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Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943
A;Accession: B70232
A;Status: preliminary; nucleic acid sequence not shown; t R; Fraser, C.M.; Casjens, S.; nuany son, D.; Peterson, J.; Kerlavage, Bowman, C.; Garland, S.; Fujil, hypothetical protein BBG10 - Lyme disease spirochete plasmid G/1p28-2 C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999 C;Accession: B70232 RESULT 10 C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hat 0, 580-586, 1997 Borrelia burgdorferi

Hatch,

₹ ? : : BES

A; Experimental source: C; Genetics: A; Molecule type: DNA A; Residues: 1-1098 <KLE> A; Cross-references: plasmid GB:AE000786; NID:g2690008; strain PIDN: AAC66075.1; translation PID:g2690032; not TIGR: BB

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surface membrane protein lmp4 - Mycoplasma hominis (fragment)
(;Alternate names: hypothetical 624 protein; Lmp4 protein
C;Species: Mycoplasma hominis
C;Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 11-Jan-2002
C;Accession: PC6003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
PC6003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Ladefoged, S.A.; Jensen, L.T.; Brock, B.; Birkelund, J. Bacteriol. 178, 2775-2784, 1996
A;Title: Analysis of 0.5-kilobase-pair repeats in the A;Reference number: JC6009; MUID:96213016
A;Accession: PC6003
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A; Residues: 1-624 <LAD>
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Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 114; Conserv
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                                                                                                                                                                                                                                                                 SVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEKR 121
                                                                                                                                                                                                                                                                                                                             APSDSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROVVVALEKOVNEYEKTALDRSFVEAQKALQK 660
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 TIQQAKTELEKE - - -
                                   TQIPALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLKNFMVNRVFIPTKKF--FN 294
                                                                                                             VDEFGASFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMD
                                                                                                                                                                                                                            EVQKANQAVASNNTASMQSAKSSLDAKVTEIT----KKLE-TFNKDKDAKFKELQQTRKN 196
                                                                                                                                                                                                                                                                                                     AQADNLARSTKEQL--NKSI-SSANTLL--AKLTD----KDNTIQQAKTELEK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -YQNLLKEKESREREIIKTLPHTDQVSALQKLNDEINEKNKAFVEKYGKSFETL--NESN 628
                                                                                                                                                    IDEFINTNKTNPNYSELISQLTSKRDSKNSVTNSSNKSDIET-ANTELKQALA--KANTD
                                                                                                                                                                                      FWMRFRRGKNHSYFHDLVFNLLEK-----NVTRDADATDIENFASRYLYMATLYYKTYTN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TVDFFNKEIRDPSKALKEKVSNDAKDLF-----ENKIGQGTVDFINNEIRD
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                                                                                                                                                                                                                                                                                                                                                                              5.6%; Score 133; DB 2; ilarity 22.4%; Pred. No. 0.39; Conservative 85; Mismatches 171.
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                                                                         -----KSAKEQL------NNSVSSANTLLAKLTDKDN
 VQKANQAVASNNTAS----
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-MQSAKSSLDAKVTEITKKLETFN
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C;Accession: S48326; S48825
R;Bowman, S;; Churcher, C.
submitted to the EMBL Data Library, Au
A;Reference number: S48326
A;Accession: S48326
A;Accession: S48326
A;Accession: S48326
A;Residues: 1-113 <BOW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references:
C;Genetics:
A;Map position: 13L
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A; Residues: 88-607 <BRO>
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                                                                                                                                                                   KKFFNKBIREPSKALKEKVSTDTKDLFENKIGQGTVDFFNKEIRDPSKALKEKVSNDAKD
                                                                                                                                                                                                                                                                                                                                      TGLFGW---
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--KEKEEEVNTKDNKAEKEEEEINKVEVTPEEPSKSIDNKAEKEEEEI
                                  IRKVYTEADDLFENKIGQGTVDFINKEI--RDPSKALIRKVSTEADNL 455
                                                                         VTENK - - - - SIEDVQEEV - - - - QGKVEGEDDGAERKTENEIENETV - - - - NKTEDKAE - -
                                                                                                                                                 ---FPEELE--STYLRINGTNEEKEIEEKE-----
                                                                                                                                                                                                                         PLDVE-----SSNESLIEMMVKRKIEVLREHV----YMSLNVFLKSFLYDTNDLEIP-
                                                                                                                                                                                                                                                          -MDTQIPALPKFAKRESL--MVVQRLLATVAGYVDTPWYKKWYMKLKNEM--VNRVFIPT
                                                                                                                                                                                                                                                                                                 TMLSGLVKLLSTNVSVNSLKKIL-QYLNSIPPFDGKTNKSLLSVFLAMRYKFITDEIASY 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GTVDFINKEIRDPSKALIRKVSTEADN 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: Z46373; NID: g587529; PIDN: CAA86507.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.48;
                                                                                                                                                                                                                                                                                                                                                                                                            -----RYLYMATLYYKT-----YTNVDEFGASFFNKLSFT 191
                                                                                                                                                                                                                                                                                                                    -GIKRALKQIIRSNLPLDIGTEHSV-----SRLQHITSSYKDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Library, October 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 127; DB 2; I
; Pred. No. 0.92;
63; Mismatches 147;
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RESULT 14
E70132
E70132
Eyechetical protein BB0261 - Lyme disease spirochete
hypothetical protein BB0261 - Lyme disease spirochete
C; Species: Borrelia burgdorferi (Lyme disease spirochete)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C: Accession: E70132
                     A;Reference number: A70100; MUID:98065943 A;Accession: E70132
                                                                                                   R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hat Nature 390, 580-586, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease
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A; Genetic code:
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A; Restlaues: 1-1830 <GLA>
A; Cross-references: GB: AE002127; (
A; Experimental source: serovar 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Species: Ureaplasma urealyticum
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Best Local
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  preliminary; nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSKALKEKVSTDTKDLFENK---IGOGTVDFFNKEIRDPSKA-LKEKVSNDAKDLFENK- 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKTLGSSKG--AAFWAKTALENDEELRKSFSNFKNT----STIVKDWLISNKRRFGSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLKN---FMVNRVFIPTKKFFNKEIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S----FTTGLFGWG--IKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIPAL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNLITSNLTSLGLDKNGYISQFLSKKDADNTNNLYKLASALASTPY--IDMVISGIQNDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASESVDSAANAYMINSDMSDYLSAVSDNFAERICSOVPKGSNCSASVSAYMSRCAKQDCL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNLDLDKNNIIGTQNISKKILYDVFRKNIINDQNLYELIKGMFH--SQLFNENKSQIKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --TLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEKRFWMRFRRGKNHSY 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Pred. No. 5
sequence
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RESULT 15
S35027
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A; Experimental source: strain B31
C; Superfamily: hypothetical protein B80261; tetratricopeptide
F;103-135/Domain: tetratricopeptide repeat homology <TT1>
F;137-170/Domain: tetratricopeptide repeat homology <TT2>
F;205-238/Domain: tetratricopeptide repeat homology <TT3>
F;205-238/Domain: tetratricopeptide repeat homology <TT4>
F;278-310/Domain: tetratricopeptide repeat homology <TT4>
F;278-310/Domain: tetratricopeptide repeat homology <TT6>
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R:Thompson, S.A.; Wang, L.L.; Sparling, P.F.
Mol. Microbiol. 9, 85-96, 1993
A;Title: Cloning and nucleotide sequence of
A;Reference number: S35026; MUID:94018616
A;Accession: S35027
                                                                                                                                                                                                                                                                                                                                                                                                            cytotoxin RTX homolog frpC - Neisseria meningitidis C;Species: Neisseria meningitidis C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 C;Accession: S35027
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A; Residues: 1-1829
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A; Residues: 1-460 < KLE>
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Matches
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                                                                                                                                                                  Local
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                                   ---DATDIENFASRYLYMATLYYKTYTNVDEFGASFFNKLSFTTGLFGWGIKRALKQIIR 208
                                                                                                         LPDPYQLEAAFILFKESDANPANSTEKRFWMRFRRGKNHSYFHDLVFNLLEKNVTRDA--
EKFDRVALQHF-SQYVDLINKNNGRLPNTSEIERSYYKAVTY----HGVSSSAAIDLVIN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRVFIPTKKFF--NKEIREPSKALKE--KVSTDTK-----DLFENKIGQ--------G
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                                                                        LGDRYADNAAAIVGKDTNLNGLN-----LWM--KKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---LKDFISKIKENKIKGLCIAPSKFSLKAKQMIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKVSTGAEDLFENKIGQGTVDFI-----NNEIRDPSKALIRKVYTEAD---DLFENKI 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEAFTKVEEIDPNYKNIKEKL-EFSKRLNENIALRIYLRSSKENFEKIANEI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVDFFNKEIRDPS-KALKEKVSNDAKDLFEN-----KIGQGTVDFINNEIRDPSKALI 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QAVIIFNNIKKNIQGDIEALLAYAKSLSKMNQDHLALEIANKI------KQKDGMI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLQHITSSYKDYMDTQIPALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLKNFMV 282
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                                                                                                                                               th 5.2%; Similarity 20.3%; 80; Conservative (
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Pred. No. 8;
53; Mismatches
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Pred. No. 1.3;
55; Mismatches
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A:Map position: segment 4
C:Superfamily: influenza virus hemagglutinin
C:Keywords: hemagglutinin; homotrimer; lipoprotein; thiolester bond
C:Keywords: hemagglutinin; homotrimer; lipoprotein; thiolester bond
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-343/Product: hemagglutinin HA1 chain #status predicted <HA1>
F:345-566/Product: hemagglutinin HA2 chain #status predicted <HA2>
F:555,562,565/Binding site: palmitate (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Virol. 49, 276-278, 1984
A;Title: Nucleotide sequence of the influenza A;Reference number: A04064; MUID:84090410
A;Accession: A04064
A;Molecule type: genomic RNA
A;Residues: 1-566 <CON>
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R; Concannon, P.; Cummings,
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C;Genetics:
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C;Species: influenza A virus
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQAAREFFKGLPSFKDLAEKFRDLFPNP--EGWID 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKEKVSNDAKDLFENKIGQGTVDFINNEIRDPSKALIRKVSTGAEDLFENKIGQGTVDFI 398
NAINGITNKVNSVIEKMNTQFTAVGKEFNK-LEKRMENLNKKVDDGFLDIWTYNAELLVL
                                    KLKNFMVNRV------FIPTKKFFNKEIREPSKALKEKVSTDTKD------L 315
                                                                                                                                                                                          TTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSS--YKDYMDTQIPALPKFAKR 248
                                                                                                                                                                                                                                                                        YFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLYYKTYTNVDEFGASF---FNKLSF 190
                                                                                                                                                                                                                                                                                                                                                   LKYPLEAKYQPLTLPDPYQLEAAFILFKESDA-----NPANSTEKRFWMRFRRGKNHS 133
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                                                                         TKLRMVTGLRNIPSIQSRGLEGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQ
                                                                                                                                                                                                                                                                                                                                                                                         ELREQLSSYSSFERFEIFPKER---SWPK-HNVTRGVTASCSHKGKSSFYRNLLWLTEKN 172
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                                                                                                                                                    NRG-FGSG-----IITSNASMDECDTKCQTPQGAINSSLPFQNIHPVTIGECPKYVRS
                                                                                                                                                                                                                                 YVSVVSSNYNRRFTPEIAERPKVRGQAGRINYYWTLLEPGDTIIFEANGNLIAPWHAFAL
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                                                                                                             -QRLLATVAGYVDTPW---YKKWY------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 121; DB 1; ; Pred. No. 2.1; 68; Mismatches 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AEKAKQVVEDLAQAAKEAYEN--AKSTAEKA 357
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RESULT
A72358
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A;Accession: D71623
A;Status
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R;Gardner, M.J.: Tettelin, H.
R;Gardner, M. Salzberg, S.;
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erythrocyte membrane protein PfEMP3 PFB0095c - malaria parasite (Plasmodium C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                             A; Title: Evidence for lateral gene transfer A; Reference number: A72200; MUID:99287316 A; Accession: A72358
                                                                                                                                                                                                                      R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                 conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C; Species: Thermotoga maritima
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                                                                      A; Molecule type: DNA
A; Residues: 1-447 < ARN>
                                                                                                                                                                                                                                                                             C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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                                 A; Experimental
                                     A;Cross-references: GB:AE001734; GA;Experimental source: strain MSB8
                                                                                                                                                                                     Nature 399, 323-329, 1999
                                                                                                                                                                                                                                                              C; Accession: A72358
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                                                                                                           A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NKELRNKGSEGLKENVYTN-NDLKNNDI--QNKDLSNKDMK--NKELLNKDISNKDMKNK 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EL-QNKGSEGLKE--NAELK--NKELQNKGSEGLKENAELKNKELQNKGSEGLKENAELK 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLFENKIGQGTVDFINNEIRDPSKALIRKVSTGAEDLFE-----NKIGQG---TVDFI 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKELQNKGSEGLKENAELKNKEL-QNKGSEGLKENAELKNKELRNKGSEGLKENAELKNK 1179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tettelin, H.; Carucci, alzberg, S.; Zhou, L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.0%;
31.4%;
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                                                      GB:AE000512;
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Pred. No. 20;
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Sutton, G.G.; Clayton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              523
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                                                                                                                                                                  between
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                                                      NID: g4981107;
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                                                                                                                                                                    Bacteria
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Query Match Best Local Similarity

5.0%; 21.8%;

Score Pred.

117.5; No. 2.

6

DВ

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Length

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Nucleic Acids Res. 29, 2145-2153, 2001

A/Title: The complete genome sequence of the murine respiratory
A/Reference number: A99512; MUID:21267165; PMID:11353084
A/Recession: H90565
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A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-986 < KUR>
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;Date: 24-May-2001 #sequence_revision
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene: MYPU_4320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
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                  411
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                                                                                                                816
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RKVYTEADDLFENKIGQGTVDFINK---EIRDPSKALIRKVSTEADNLLE : | :| | :| :| :| :| :|
                                                                                                                                                                                                KFA----KRESLMVVQRLLATVAGYVDTPWYKKWYMKLKNEMVNRVEIPTKKFENKEI-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YVDTPWYKKWYMKLKNEMVNRVFIPTKKEFNKEIREPS-----KALKEKVST
                                                                                                             YPNNRLTYEDTLSEIDKHIQLIKNNYNQGKI----NQKEYEIFLLLVQKWKNEIKNFFIKK
                                                                                                                                         EPSKAL--KEKVSTDTK--DLFENKIGQGTVDFFNKEIRDPSKALKEKVSNDAKDLFENK 354
                                                                                                                                                                          KYANEIKKNLSTNEKEKISYEVLNSIDISNIKFAY - - - KEMIIDEIYLENLLFFNKKISK
                                                                                                                                                                                                                                        NIYDEKNNEIFRNISLENKKKYLKNLSQVSNIFSSLKTFKEYGKNEKISDFSLEQLNQYQ
                                                                                                                                                                                                                                                                       GIKRALKQIIRSNLPLDIGTEH--SVSRLQHITSSYK-------DYMDTQIPALP
                                                                                                                                                                                                                                                                                                     FSLEEQSIN----DAFKIYANSSDKEIQQLVYGEKYEQVVEDFINEWNSLKISFS-----
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                                                --DKSLD--EKEFIDYGKRILKSVFQKVKNQIEAMWLEKILKEYHGINNDQIRKDWKKRI
                                                                             IGQGTVDFINNEIRDPSKALIR----KVSTGAEDLFENKIGQGTVDFINNEIRDPSKALI
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R; Dietrich, F.
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A;Map position: 5L C;Superfamily: kinesin-related protein CINB; kinesin motor domain homology C;Superfamily: kinesin-related protein CINB; kinesin motor domain homology C;Keywords: ATP; coiled coil; microtubule binding; mitosis; nucleotide binding; E;75-520/Domain: kinesin motor domain homology #status atypical <KMOT> F;166-173/Region: nucleotide-binding motif A (P-loop)
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A; Residues: 1-253,'A',255-830,'H',832-1038 <HOY>
A; Cross-references: EMBL:Z11859; NID:g3541; PIDN:CAA77885.1;
A; Cross-reference extracted from NCBI backbone (NCBIN:107723,
A; Note: sequence extracted from NCBI backbone (NCBIN:107723,
R; Rousselet, G.; Simon, M.; Ripoche, P.; Buhler, J.M.
submitted to the EMBL Data Library, May 1994
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A;Accession: S69009
A:Status
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A;Title: A second nitrogen permease regulator in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Description: A second nitrogen permease regulator in A;Reference number: S44938
A;Accession: S44939
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A;Molecule type: DNA
A;Residues: 1-1038 <DIE>
A;Cross-references: EMBL:U18795; NID:g603241;
A
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A; Residues: 1021-1038 < ROW>
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A; Residues: 1021-1038 < ROU>
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J. Cell Biol. 118, 109-120, 1992
A;Title: Two Saccharomyces cerevisiae kin
A;Reference number: A42641; MUID:92317149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Description: The sequence
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C; Species: Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                    KKLRIFDSSTANNTTSNSASSSRSNSRNSSPRSLNDLTPKAALLRKRLRTKSLPNTIKQQ 307
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MEGLNLLQKGLKHRQVÄSTKMNDFSSRSHTIFTITLYKKHQDELFRISKMNLVDLAGSEN
                                                                                         ---FNLLEKNYT-RDADATDIENFASR--YLYMATLYYKTY--
                                                                                                                                                                                  YQQQQAVNSRNNSSSNSGSTTNNASSNTNTNNGQRSSMAPNDQTNGIYIQNLQEFHITNA 367
                                                                                                                                                                                                                                                                           YQLEAAFILFKESDANPANSTE-----
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er, J.M.
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R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B., P. L.; H.; Qin, H.; Vamahhevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:20175755
A;Accession: E81086
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C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: E81086
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A:Residues: 1-1829 <TET>
A:Cross-references: GB:AE002490;
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                                                                                FAKRESLMVVQRLLATVAG--YVDTPWYK--KW----YMKLKNEMVNRVFIPTKKEENKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB:AE002098; NID:g7226651; PIDN:AAF41776.1; PID:g722669 B, strain MC58
                                                                                                                                                                                                                                             ----NVDEFGASFFNKLSFTTGLFGWGIKRA
    -TDTKDLFENKIGQGTVDFFNKEI 332
                                                                                                                                                                                                                                                                                                                                                                   150;
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A;Residues: 1-2166 <KLE>
A;Cross-references: GB.AE001153; GB:AE000783; NID:g2688419;
A;Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943
A;Accession: G70163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein BB0512 - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALFESIDSSSSKFE-NQMESKYKS-----FTDKLTAGMDEFSLMYGEKFETLSQEATNNY 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCSASVSAYMSRCAKQDC 75
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                                          LESYYLEKIDEFRNQGAIYSDELLQDIMNHFNKETRELEENLSKKFAAVLNNSEEFVKEV
                                                                                  IRKVYTEADDLFEN----
                                                                                                                        RKDSINNEVDSKLSDWQSKLNEITVKIENLLSS--GKVDLDLIDSEVTTKIKELKFSIES
                                                                                                                                                              --DFINNEIRDPS---KALIRKVSTGAEDLFENKIGQGTVDFINNEIRDPSKAL-----
                                                                                                                                                                                                      --CDYKLKDFKIESEDILNNFKSDLNEFIESKLQIVSNIKSDNQKQIDDFLDRISKDILN
                                                                                                                                                                                                                                          GTVDFFNKEIRDPSKALKEKVSNDAKDLFENKI------GQGTV---
                                                                                                                                                                                                                                                                                     --YKELKDMSYSQSDEAILGIKEFINRQTEIIKDKSVFMLEDLNKKFDDKNNFVISKIEE
                                                                                                                                                                                                                                                                                                                         KWYMKLKNEMVNR---VEIPTKKEENKE---IREPSKALKE---KVSTDTKDLFENKIGQ
                                                                                                                                                                                                                                                                                                                                                                   IKVSSEELLSSATLKIESLEKDVNDRMEYVLLKTGDIESLVIEK---
                                                                                                                                                                                                                                                                                                                                                                                                         LDIGTEHSVSRLQ-HITSSYKDYMDTQIPALPKFAKRFSLMVVQRLLATVAGYVDTPWYK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---TNEEFLSLIQIQKDKGIELSESVFNDLSDHIQKKAIDMHGSW--KDELIALNKSLLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --GKNHSYFHDLVFNLLEKNVTR--------DADATDIENFASRYLYMATLYY 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEFQDLNKKLE-----NEIESFYNMFEK----TQETLKVDFNTSLINIKD
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19.3%; Pred. No. 21;
                                                                              -KIGOGTVDFINKEIRDPSKALIRKVST
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PID:9268

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                                                                            R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views A;Reference number: A82870
A;Accession: G82925
                                                                                                                                                           hypothetical protein UU162 [imported] - Ureaplasma urealyticum c;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change C;Accession: G82925
                                                                                                                                                                                                                         RESULT
G82925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: G97085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sensory transduction histidine kinase (with HAMP domain) [imported] - Clostridium C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: G97085
                               A; Molecule type: DNA
A; Residues: 1-457 <GLA>
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 A;Cross-references: GB:AE002116; (A;Experimental source: serovar 3;
                                                              A; Status: preliminary
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A; Residues: 1-473 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VORLLATVAGYVDTPWYKKWYMK------LK-NFMVNRVFIPTKKFFNKE 296
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                                                                                                                                                                                                                                                                                                          ADDLFENKIGQGTVDFINKEIRDPSKALIRKVSTE 451
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GB:AF222894; NID:g6899118; PIDN:AAF30568.1; GSPDB:GN001; biovar 1
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Pred. No. 3.
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A;Title: The genome sequence of the food-borne A;Reference number: A81250; MUID:20150912
A;Accession: E81339
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                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1250 <PAR>
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A;Genetic code:
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Pred. No. 12;
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probable restriction /modification enzyme Cj0690c [imported] - Campylobacter C;Species: Campylobacter jejuni C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000 C;Date: 31-Mar-3000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000 C;Date: 31-Mar-3000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000 C;Accession: E81339 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead Nature 403 665-669 2000
                                                                                                                                                                                                       134 YFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLYYKTYTNVDEFGASFF-----
LIQSALKDKLNNENILKFKILDNACGSGHFLVGVLNAITHIVLSDFDHFTNLKELYEEEK
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                                                                                                                                   YFDNYDFKILEK-----SKKVEKYT--FYKKGQIYLKNTSNSRKASASFYTPQSIANF
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                                                                   -----NKLSFT-----TGLFGWGIKRALKQIIRSNLP-----LDIGTEHS 220
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A;Title: Genomic sequence comparison of two unrelated isolates of the A;Reference number: A71800; MUID:99120557
A;Accession: H71931
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C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision
C;Accession: H71931
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C;Superfamily: Helicobacter pylori hypothetical protein jhp0440
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A; Residues: 1-912 < ARN>
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                                                                                                              KLKNF-MVNRVFIPTKKFFNKEIRE---PSKALK----
                                                                                                                                                                                                                                                                DLPIILHDGQVIAGNHRIAGMLNFTPKSRYIYNKAIKEYYRIDLKPDELLVRVPHQRLDN
                                                                                                                                                                                                                                                                                                                          YDLDYAIV--KAKDLKPSFTTGGTQKRTDM-----NEEQIKSIAENFDPKKIFGSGGFE
                                                                                                                                                                                                                                                                                                                                                     YQLEAAFILFKESDANPA---NSTEKRFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADAT
 NKIGQGTVDFIN---NEIRD
                                                                                      DIKSYEKVKKMFVDNAGSFHNLIHDMNFPNVSLNAYLSDIMDRSFANLKNYPSTSESLKD
                                                                                                                                                ATHPNVG-
                                                                                                                                                                          GTEHSVSRLQHITSSYKDYMDTQIPALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYM
                                                                                                                                                                                                       TEINNLAASSNQGRENSESDHAIAVLSHYEAKLKELDKKLDADSIYSLKNIVAKNLNFDK
                                                                                                                                                                                                                                      SFFNKL--SFTTGLFGWGIKRA----
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                           LSEKFYKTSSLDMFEKSDQSASDISEILGGAIARFARFDDPSKALFESLKSDNIKKGLKD
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                                                                                                                                                                                                                                                                                             -NFA--SRYLYMATL--YYKTYTNVDE----
                                                                                                                                                                                                                                                                                                                                                                                   51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D.T.; King, B.L.;
D.; Mills, S.D.;
                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                          Score 115;
                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NID:g4154971; PIDN:AAD06018.1; PID:g41549
                                                        EIRDPSKALKEKVSND--AKDLFE
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                                                                                                                                                                                                                                                                                                                                                                                   167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brown,
                                                                                                                                                                                                                                                                                                                                                                                                            Length 912;
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                                                                                                                                                                                                                                   -LKQIIRSNLPLDI
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                                                                                                                                              ---NRWQKEFSN
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PSKA
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HsdR1 protein - Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Date: 29-Nov-1995 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A: Residues: 1-986 <DYB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Microbiol. 12, A; Title: Regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: S49394
R; Dybvig, K.; Yu, H
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Best Local :
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ND--KDLDDIEKS-----EFIKKWSRRSKEVDKDIIDKLSIEYKESIE
                   RKVYTEADDLFENKIGQGTVDFINK---EIRDPSKALIRKVSTEADNLLE
                                                                                                                       YPNNRLTYEDTLSEIDKHIQLIKNNYNQGKI----NQKEYEIFLLLVQKWKNEIKNFFIKK
                                                                                                                                                                                                                 KEA----KRESLMVVQRLLATVAGYVDTPWYKKWYMKLKNEMVNRVEIPTKKEENKEI-R
                                                                                                                                                                                                                                                  NIYDEKNNEIFRNISLENKKKYLKNLSQVSNIFSSLKTFKEYGKNEKISDFSLEQLNQYQ
                                                                                                                                                                                                                                                                               GIKRALKQIIRSNLPLDIGTEH--SVSRLQHITSSYK-------DYMDTQIPALP
                                                                                                                                                                                                                                                                                                                FSLEEQSIN---DAFKIYANSSDKEIQQLVYGEKYEQVVEDFINFWNSLKISFS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YKIADITKDMFNPDSKEFKDIDIYDFTHYLLMVNREPNENNPVLNRLIQAVKGMQKESEK
                                                                                        IGQGTVDFINNEIRDPSKALIR----KVSTGAEDLFENKIGQGTVDFINNEIRDPSKALI
                                                                                                                                                     EPSKAL--KEKVSTDTK--DLFENKIGQGTVDFFNKEIRDPSKALKEKVSNDAKDLFENK
                                                            --DKSLD--EKEFIDYGKRILKSVFQKVKNQIEAMWLEKILKEYHGINNDQIRKDWKKRI
                                                                                                                                                                                     KWANEIKKNLSTNEKEKISYEVLNSIDISNIKFAY---KEMIIDEIYLENLLFFNKKISK
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2, 547-560, 1994
on of a restriction and or: S49391; MUID:95020589
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Мус

myosin-like protein MLP1 - yeast (Saccharomyces cerevisiae) N;Alternate names: protein YKR095w; protein YKR415 C;Species: Saccharomyces cerevisiae C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change C;Accession: S38173; S40647; S31207 R;Baladron, V; Ballesta, J.P.G.; Bou, G.; del Rey, F.; Esteban, submitted to the Protein Sequence Database, March 1994 A;Reference number: S38158

Esteban,

P.F.; Garcia-Cantale

21-Jul-2000

A; Molecule type: DNA A; Residues: 1-1875 <AAL> A; Cross-references: EMBL: Z283; A; Experimental source: strain

EMBL:Z28320; NID:g486586; ce: strain S288C

PID:g486587;

MIPS:YKR095w

A; Accession: S38173

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R;Bou, G.; Esteban, P.F.; Baladron, V.; Gonzalez, G.A.; Cantalejo, J.G.; Remacha, Yeast 9, 1349-1354, 1993

A;Title: The complete sequence of a 15 820 bp segment of Saccharomyces cerevisiae A; Reference number: $40644; MUID:94205265

A; Accession: $40647

A; Molecule type: DNA
A; Residues: 1-1875 <BOU>
A; Cross-references: EMBL:X73541; NID:9450550; PIDN:CAA51948.1; PID:9450554
A; Experimental source: strain $288C
R; Koelling, R; Nguyen, T; Chen, E.Y.; Botstein, D.
MOl. Gen, Genet. 237, 359-369, 1993
A;Title: A new yeast gene with a myosin-like heptad repeat structure.
A; Reference number: $31207; MUID:93247549
A; Accession: $31207; MUID:93247549
conserved hypothetical protein SA1085 [imported] - Staphylococcus aureus (strain C;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: E89897
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A; Residues: 1-300,'A',302-1875 <KOE>
A; Cross-references: EMBL:L01992; NID:g171958; PIDN:AAA34783.1;
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESETVNEAKEAIITLKSEKMDLESRIEEL----QKELEELKTSVPNEDASYSNVTIKQLT
                                                                                                                                                                                                                                          -----LNNELDLQKKGMEKE---KAD--FKKRI--SILQNNNKEVEAVKSEYESKLSK 102
                                                                                                                                                                                                                                                                                                                                                                                                    ----QTDIEKLQYKVKSLEKEIEEDKIRLHTYNVMDETINDDSLRKELEKSKINLTDAYS
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Pred. No. 24;
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A; Residues: 1-652 <KUR>
A; Cross references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E89897
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                                                                                                                                                                                                                                                                                                                                                        R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer Nucleic Acids Res. 29, 2145-2153, 2001.
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: F90561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein MYPU_3980 [imported] - Mycoplasma pulmonis (strain UAB C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
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                                                                                                                                                                                                  A;Genetic
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                                                                                                                                                                                                                                                             A; Experimental source:
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A;Experimental source: strain N315
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A; Residues: 1-868 < KUR>
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                                                                                                                                      Local Similarity
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                                         IALSSLLERYEEKVKLIYIDPPYYEEDK----KEENTFLYNSNFKLSTWLSFMK-----
                                                                            LTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEK-RFWMRFRRGKNHSY 134
FHDLVFNLLE--KNVTRDADATDIENFASRYLYMATLYYKTYTNVDEFGASFFNKLSFTT 192
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                                                                                                                     Conservative
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; Pred. No. 7.1;
75; Mismatches
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Pred. No. 9.5;
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A;Molecule type: DNA
A;Residues: 1-2116 <WAR>
A;Residues: 1-2116 <WAR>
A;Cross references: GB:M14628; GB:M11938; NID:g167834; PIDN:AAA33227.1;
A;Cross references: GB:M2628; GB:M11938; NID:g167834; PIDN:AAA33227.1;
R;DeLozanne, A.; Lewis, M.; Spudich, J.A.; Leinwand, L.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 6807-6810, 1985
A;Reference number: A24728; MUID:86016788
A;Accession: A24728
                                                                                                                                                                                                                                                                                                                                                                                                                                                      myosin heavy chain [similarity] - slime mold (Dictyostelium discoideum) N;Contains: myosin ArPase (EC 3.6.1.32) C;Species: Dictyostelium discoideum C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 02-Feb-C;Accession: A2655; A24728; S00250 R;Warrick, H.M.; De Lozanne, A.; Leinwand, L.A.; Spudich, J.A. Proc. Natl. Acad. Sci. U.S.A. 83, 9433-9437, 1986
                                                                   F;89-747/Domain: myosin motor domain homology F;179-186/Region: nucleotide-binding motif A (F;819-2116/Domain: alpha-helical rod <ROD>
                                                                                                                                                                                               A;Title: Phosphorylation of threonine residues on A;Reference number: S00250; MUID:88112226
A;Accession: S00250
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 2035-2116 <DEL>
R; Wagle, G.; Noegel, A.; Sch
FEBS Lett. 227, 71-75, 1988
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                 77;
                Score 113.5;
Pred. No. 35;
77; Mismatches
                                                                                                                                                                                                                                                                      J.; Gerisch,
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                166;
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                121;
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                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:X60550
A;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNĀ
A; Residues: 1-2364 <ZAU>
                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                   TNKDKAELILPNGQEVDIP --
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                                                                                                                                                                                                                                                        Conservative
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R;Zauner, W.; Kratz, J.; Staunton, J.; Feick, P.; Wi
Eur. J. Cell Biol. 57, 66-74, 1992
A;Title: Identification of two distinct microtubule
A;Reference number: A56577; MUID:92347374
A;Accession: A56577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             microtubule-associated protein MAP 1B - rat (fragment) C;Species: Rattus norvegicus (Norway rat) C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #te
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Note: nucleotide sequence not given; conceptual translation C; Superfamily: microtubule-associated protein MAP1B
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AKRFSLMVVQRLLAT---VAGYVDTPWYKKWYMKLKNFMVNRVFI--PTKKFFNKEIREP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRNTLEKLKKKYEEELEEMKRVNDGQSDTISRLEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AREQRISEIIKAIQAATRGWIAR-----KVYKQAREHTVAA-------RIIQQNLRA
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                                                SVSSLIVWHPANPAEKIIRVLFPGN-STQYNILEGLEKLKHL----
                                                                                           FTTGLFGWGIKRALKQIIRSNLPLDIGTEHSV----SRLQHITSSYKDYMDTQIPALPKF
                                                                                                                                                                                            KNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLYYKTYTNVDEFGASFFNKLS
                                                                                                                                                                                                                                             QYLN-KLSMKPEPLFRSVGNAIEPV-ILFQKMGVGKLKMYVLNPVKSSKEMQYFMQQWTG
                                                                                                                                                                                                                                                                                           QSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDA--
                                                                                                                                                                                                                                                                                                                                              ESQGSTSNSDWMKNLTSPDLGVVFLNVPENLKNPEP---
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20.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 113.5;
Pred. No. 40;
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A;Map position: 4
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A; Residues: 1-1314 <STO>
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A;Accession: A85176
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:NC_001268;
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Best Local Similarity
Matches 99; Conserv
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TGAEDLFENKIGQGTVDFINNEIRDPSKALIRKVYTEADDLFENKIGQGTV-DFINKEIR
                                       SNFRVLAV-DIIPLLISSLGNPLGDISSENGLKDSWGLGCIDALVQRCSDTS-ALIR---
                                                                                       ELKKVVSNLPKFLVHKA--PEKAEPRGFAVEAVLEIVKAMEVEGQSEFVD-FVMKMCQGK
                                                                                                                                                                                          --- LEKLGSVLSFVHLDREPDSL-----KSLVQTV-SEIPL-LALEHSGVLNYDRLMEM
                                                                                                                                                                                                                                                                  ANSTEKRFWMRFRRGKNHSYFHDLVFNLLEKNV-TRDADATDIENFASRYLYMATLYYKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKD 640
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                                                              VDFFNKEIRDPSKALKEKVSNDAKDL-----FENKIGQGTVDFINNEIRDPSKALIRKVS
                                                                                                              WYKKWYMKLKNEMVNRVFIPTKK----FENKEIREPSKALKEKVSTDTKDLFENKIGQGT
                                                                                                                                         CGKILGGVLNSDHGDMALTAAEISKSLTPLLLMGKHQARSFALGFVSRKLMSLA--KDNP
                                                                                                                                                                                                                YTNVDEFGA--SFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHS----VSRLQHI
                                                                                                                                                                                                                                           GSNSQREKGNKKKRGRG------KRNLGYEDGEETEEGGFDAKLMFIV-----
                                                                                                                                                                                                                                                                                            SGRLAILASDAYLSLLLSTNC-----PVFTFFSPIAFLSLLGSIRRYLKRRDDSAGQ
                                                                                                                                                                                                                                                                                                                   KGSNCSASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANP 114
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20.2%; Pred. No. 22;
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A; Molecule type: DNA
A; Residues: 1-1957 <CON>
A; Cross-references: EMBL: Z70690; PIDN: CAA94624.1;
A; Cross-reference: strain 972h-; cosmid clf3
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                                                   717
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R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, April 1996 A; Reference number: Z21767 A; Accession: T38077 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 34
T38077
R:Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
QK--ESTLSDENNDLRTKLLKLEESNKSLIKK-QEDVDSLEKN-----IQTLKEDLRKS
                                                                                                                                                                                                                                                                                                     KSALID-----KKDQELNNL---REQIKEQKKVSESTQSSLQSLQRDILNEKKKHEVYES
                                                                                                                                                                                                                                                                                                                                                                                                                                  QI--IRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIPALPKFAK--RFSLMVVQRLLAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAFILFKESDANPANSTEKRFWMRFRRGK------NHSYFHDLVFNLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSASVSAYMSRCAKQDCLTLQ------SLKYPLEAKYQPLTLPDPYQLE 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVTKTLLAASESVDSAANAY-MINSDMSDYLSAVSDNFA------ERICSQVPKGSN 58
                                                 NKIGQGTVDFINNEIR-----DPSKALIRKVYTEADDLFENKIGQGTVDFINKEIRDP
                                                                                                  SVMQLKENEQNFSSLDTSFKKLNESHQELENNHQTITKQLKDTSSKLQQLQLERAN--FE
                                                                                                                                                                                                  QLNELKGELQTEISNSEHLSSQLSTLAAEKEAAVATNNELSESKNSLQTLCNAFQEKLAK
                                                                                                                                                                                                                                                 VAGYVDTPWYKKWYMKLKNEMVNRVFIPTKKEFNKEIREPSKALKEKVSTDTK--DLFEN
                                                                                                                                                                                                                                                                                                                                                                                                   QLEEARSSL-----AHATGKLAEINSE-RDFQNKKIKDFEKIEQDLRACLNSSSNELKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNRTIHSQLTDAESKLSSF---EQENKSLKGSIDEYQ----NNLSSKDKM----VKQVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLSTRISEFD----NLKSERDTLSIKNEKLEKLLRNTIGSLKDSRTSNSQLEEEMVELKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTVSTLRQTENSLRAECKTLQEKLEKCAINEEDSKLLEELKHNV-ANYSDAIVHKDKLIE
                                                                                                                                              ----KIGOGTVDFINN-----EIRDPSKALIRKVSTGAEDLFE
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probable spindle pole body component, probable gamma-tubulin interacting protein, yeast C;Species: Schizosaccharomyces pombe C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000 C;Accession: T50382 R;Saunders, D.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
                                                                                                                                                           RESULT 36
G90576
heat shock atp-dependent proteinase [imported] - Mycoplasma pulmonis (strai C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: G90576
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A;Accession: T50382
A;Status: preliminary; translated from
A; Molecule type: DNA
A; Residues: 1-842 <K
A; Cross-references:
                                                R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; (Nucleic Acids Res. 29, 2145-2153, 2001)
A;Title: The complete genome sequence of the murine respiratory A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: G90576
A;Status: preliminary
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A; Residues: 1-566 <SAU>
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                                                                                                                                                                                                                                                                                                                                              VDFIN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQGDVVWKGKYFLDKELIPSFLSEELVDKIFLIGKSLNFARYGCGDFDW----AQEHYQK
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                <KUR>
GB:AL445566; PID:g14089933; PIDN:CAC13692.1;
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Pred. No. 8.6;
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                                                                                                                                          Galisson, F.;
                                                                                                      pathogen
GSPDB:GN00153
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A; Experimental source: strain UAB C; Genetics:
A; Genet MYPU_5190
A; Genetic code: SGC3
C; Superfamily: ATP-dependent serin
                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Saccharomyces cerevisiae
C;Date: 21-Sep-1993 #sequence_revision 03-May-1994
C;Accession: A46417; S53979; S53902
R;Gu, Z; Woerschell, R.P.; Sherman, F.; Goldfarb, |
Proc. Natl. Acad. Sci. U.S.A. 89, 10355-10359, 1992
A; Molecule type: DNA
A; Residues: 1-110,'V',112-582,'Q',584-602 <CHU>
A; Cross-references: EMBL: Z54141; NID: g1072408;
                                                                                             R;Churcher, C.M. submitted to the EMBL
                                                                                                                                A; Molecule type: DNA
A; Residues: 571-582, 'Q', 584-640, A; Cross-references: EMBL:Z49212;
                                                                                                                                                                                                         R:Connor, R.; Churcher, C.M. submitted to the EMBL Data Library, A:Reference number: S53969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIP1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: nuclear import protein; protein YM9924.01c;
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A; Residues: 1-812 <GU1>
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A; Accession: A46417
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                                                                                                                                                                                            A; Accession: S53979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           407 DKQITHNVPILALVGPPGTGKTSLAMAIAESINKEF---VKISLGGVKDEAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 KIVAQNPSKGNIKVTLLPFKRVKVNKITISETNLSHKVMVDYSPFELVAPDPTKGKILYN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 RICSQVPKGSNCSASVSAYMSRCAKQDCLTLQSLKYPLEAKYQP--LTLPDPYQLEAAF-
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97; Conservative
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PID:g984682; MIPS:YMR309c

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C: Species: Cae
C: Date: 15-Oct
C: Accession: 7
                                                                                  A:Map position: 1
A:Introns: 17/2; 164/3; 199/1; 245/3; C:Superfamily: Caanorhabditi
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A;Residues: 1-1188 kMIL>
A;Cross-references: EMBL:279752; P
A;Experimental source: clone D2005
                                                                                                                                                                                                                    submitted to the EMBL Data A; Reference number: Z19258 A; Accession: T20333
                                                                                                                                                                                                                                                                                   hypothetical protein D2005.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t
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A; Map position: 13R
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                             Best Loc
Matches
                                                                               Introns: 17/2; 164/3; 199/1; 245/3; 366/3; 399/2; 414/3; 475/3; 526/3; Superfamily: Caenorhabditis elegans hypothetical protein D2005.4
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90; Conser
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97; Conserv
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                                         4.7%; Score 110.5;
18.5%; Pred. No. 26;
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                                                                                                                                                               PIDN:CAB02083.1; GSPDB:GN00019;
                          Pred. No. 26;
7; Mismatches
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Pred. No. 16;
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A; Residues: 1-6359 <KON>
A; Cross-references: EMBL
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VGDVTKTLLAASESVDSAANAYMINSDMSDYLSA----
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                                         Conservative
                                                     4.78; 20.58;
                                          58;
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A;Gene: bacc
A;Gene: bacc
C;Superfamily: acetate--CoA ligase homology; acyl carrier protein homo
C;Keywords: carrier protein; phosphopantetheine; phosphoprotein
F;505-946/Domain: acetate--CoA ligase homology <ACL1>
F;964-1032/Domain: acyl carrier protein homology <ACL2>
F;1542-1978/Domain: acyl carrier protein homology <ACP2>
F;1996-2063/Jomain: acetate--CoA ligase homology <ACL3>
F;3046-3483/Domain: acetate--CoA ligase homology <ACL3>
F;3046-3483/Domain: acyl carrier protein homology <ACL4>
F;3500-3568/Domain: acyl carrier protein homology <ACL4>
F;4078-4509/Domain: acyl carrier protein homology <ACL4>
F;5593-6032/Domain: acyl carrier protein homology <ACP5>
F;6050-618/Jomain: acyl carrier pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Konz, D.; Klens, A.; Schorgendorfer, K.; Marahiel, M.A. Chem. Biol. 4, 927-937, 1997
A;Title: The bacitracin biosynthesis operon of Bacillus licheniformis A;Reference number: Z21058; MUID:98089193
A;Accession: T31679
                                                                                                                                                                                                                                                                                           F;5593-6032/Domain: acetater-von tayour monology <ACP5> F;6050-6118/Domain: acyl carrier protein homology <ACP5> F;3532/Binding site: phosphopantetheine (Ser) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacitracin synthetase 3 - Bacillus licheniformis
c;Species: Bacillus licheniformis
C;Date: 29-Oct.1999 #sequence_revision 29-Oct.1999 #text_change
C;Accession: T31679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated from GB/EMBL/DDBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YKKWYMKLKNEMVNRVFIPT-KKEFNKEIREPSKALKEKVSTDTKDLFENKIGQGTVDFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLPVVSDV-EDASSADSGKDNPESMYFQVVSTIRFGQRDGIMDRLAAFLS-VTSNTGEHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVVASSVISEEVLKEESTGDCVKTSKDHMDSETAGNCSDSVINDEPVEAEDPDNVKVERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SKALIRKVSTG-----AEDLFENKIGQGTVDFINN----EIRDPSKALI-RK 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGDAEKCEESEEVTTKASSDAKEGVIAVDAVAAEPDIVQENAT - - - STDDANNEDQEKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKN---LLRHFTIKIKFLTSHKKIDKEELKEDTKQSKE-----DSKVPEKSPEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDVTSYLHLAKLPTAWPNYCNLDVIEKTVSDHIPQEVVRTQLYEAMKKYAAEMP-IDENW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GHHWFSIF----FLSHRFDILKFSTTI------AQLPWSSADIWNEEKKDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATLYYKTYTNVDEFGASFFNKLSFTTGLFGWGIKRALKQIIRSNLP---LDIGTEH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FKESDANPANSTEKRFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISLEP-----TLRFAMRCVDAKKYQTMAVDVLKFLARPQMKRMKLPNEFFEDLIVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSQVPKGSNCSASVSAYMSRCA----KQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFIL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SVSRLQHITSSYKDYMDTQI-----PALPKFAKRFSLMVVQRLLATVAGYVDTPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: AF007865; NID: g4464275; PID: g2982196;
                                                                                                                                             Score 110.5; I
Pred. No. 2.2e
68; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- QFIDYFLNLVETLRKENGIVIDEKKIVDKWANM
                                                                                                                                        1.2e+02;
nes 173;
                                                                                                                                                                                                                                              DB 2;
----VSDNFAERICSQVPKGSN 58
                                                                                                                                                                                                                                              Length
                                                                                                                                                  Indels
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                                                                                                                                             223;
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ps 24;	4.7%; Score 110; DB 1; Length 566; cal Similarity 20.8%; Pred. No. 11; 97; Conservative 67; Mismatches 171; Indels 132; Ga
	A; Map position: segment 4 C; Superfamily: influenza virus hemagglutinin C; Superfamily: influenza virus hemagglutinin C; Keywords: hemagglutinin; homotrimer; lipoprotein; thiolester bond C; Keywords: hemagglutinin; homotrimer; lipoprotein; thiolester bond C; Keywords: hemagglutinin HAl chain #status predicted <hal> F; 18-343/Product: hemagglutinin HAl chain #status predicted <hal> F; 345-566/Product: hemagglutinin HAl chain #status predicted <hal> F; 555, 562, 565/Binding site: palmitate (Cys) (covalent) #status predicted</hal></hal></hal>
209-268,'M',270-3	s: subtype H1 on: A90830 e type: genomic RNA i: 18-145,'N',148-155,'E',157-199,'P',201-203,'E',205-207,'L',
glutinin (Hl subt	417-427, 1982 The antigenic structure of the infl
PID:g62291	un: A3202 e type: genomic RNA s: 1-566 <win> eferences: GB:V01088; GB:J02143; NID:g62290; PIDN:CAA24272.1; A.J.; Brownlee, G.G.; Yewdell, J.W.; Gerhard, W.</win>
luenza virus H1 su	Nucleotide sequence of the haemagglutinin gene of a human inf nucleotide sequence of the haemagglutinin gene of a human inf consuber: A93262; MUID:82013600
1999	8-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 28-May- on: A93262; A90830; A04063 G.; Fields, S.; Brownlee, G.G. '2, 72-75, 1981
	RESULT 40 HMIV hemagglutinin precursor - influenza A virus (strain A/PR/8/34) C;Species: influenza A virus
	Qy 381 GAEDLFENK-IGQGTVDFINNE 401
2389	2330 LTGARDITGENKLKVMMEGHGREDILEGVDITRTIGWFTTMYPVLLDAGEEKALSQQIKM
300	344 SUNDARDI E-BURTGOGTUDETUN-ETDURGETAITERING
343	Qy 286 -FIPTKKFFNKEIREPSKALKEKVSTD-TKDLFENKIGQGTVDFFNKEIRDPSKALKEKV :
285 2277	Qy 240 PAL
239 2229	Oy 205 QIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQI : : : : : : : : : : : : : : : : : : :
204 2169	Qy 185 FNKL
184	Qy 147
146 2058	Qy 119 EKRFWMRFRRGKNHSYFHDLVFNLLEKN
118	Qy 59 CSASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANST:
1951	1897: LGEIENQLLKL-DKIDEAAVIARKDDDHSDYLCAYIVSKEDWTSTEISEWLEKELP

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                 362 F---INNEIRDPSKALIRKVSTGAEDL----FENKIGQGTVDFINNE 401
                                             432 FLDIWTYNAELLVLLEN---ERTLDFHDSNVKNLYEKVKSQLKNNAKE-----IGNGCFE 483
                                                                                                                                          313 HPVTIGECPKYVRSAKLRMVTGLRNIPSIQSRGLEGATAGFIEGGWTGMIDGWYGYHHQN 372
                                                                                                                                                                                                                                       204
                                                                                                                                                                                                                                                                                      158
                                                                                                                                                                                        260
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                                                                                                                                                                                                                                      TKD------LFENKIGQGTVDFFNKEIRDPSKALKEKVSNDAKDLFENKIGQGTVD 361
                                                                                                                                                                                        EANGNLIAPRYAFALSRGFGSG-----IITSNASMHECNTKCQTPLGAINSSLPFQNI 312
                                                                                                                                                                                                                                                                                                    KQD-----CLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDA------NPANST 118
                                                                                                                                                                                                          EFGASFF-NKLSFTTGL-FGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSS--YKDY 234
                                                                                                                                                        MDTQIPALPKFAKRFSLMVV------QRLLATVAGYVDTPW---YKKWY-----
                                                                                                                                                                                                                                                                                     KSSFYRNLLWLTEKEGSYP------KLKNSYVNKKGKEVLVLWGIHHPSNSK 203
                                                                                                                                                                                                                                                                                                                                  157
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Search completed: October 19, 2002, 07:52:25 Job time : 55 secs

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